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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/839,164

DATE: 01/22/2002

TIME: 17:02:42

Input Set : A:\09839164.txt

Output Set: N:\CRF3\01222002\I839164.raw

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: KOZLOV, VLADIMIR

TSYRLOVA, IRENA

(ii) TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
USES THEREOF

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.

(B) STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR

(C) CITY: ARLINGTON

(D) STATE: VIRGINIA

(E) COUNTRY: U.S.A.

(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 1.44 Mb diskette

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: MS Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/839,164

(B) FILING DATE: 23-Apr-2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/477,668

(B) FILING DATE: 07-JUN-1995

(A) APPLICATION NUMBER: US 08/316,424

(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: PCT/US94/03349

(B) FILING DATE: 29-MAR-1994

(A) APPLICATION NUMBER: US 08/040,942

(B) FILING DATE: 31-MAR-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62	GTGCTGTCTC	CTGCCGACAA	GACCAACGTC	AAGCCCGCCT	GGGGTAAGGT	CGGCGCGCAC	60
64	GCTGGCGAGT	ATGGTGGCGA	GGCCCTGGAG	AGGATGTTCC	TGTCCTTCCC	CACCACCAAG	120
66	ACCTACTTCC	CGCACTTCGA	CCTGAGCCAC	GGCTCTGCC	AGGTTAAGGG	CCACGGCAAG	180

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68 AAGGTGGCCG ACGCGCTGAC CAACGCCGTG GCGCACGTGG ACGACATGCC CAACGCCGTG      240
70 TCCGCCCTGA GCGACCTGCA CGCGCACAAAG CTTGGGTGG ACCCGGTCAA CTTCAAGCTC      300
72 CTAAGCCACT GCCTGCTGGT GACCCGTGCC GCCCACCTCC CCGCCGAGTT CACCCCTGCG      360
74 GTGCACGCCT CCTGGACAA GTTCCTGGCT TCTGTGAGCA CCGTGCTGAC CTCCAAATAC      420
76 CGT                                         423

79 (2) INFORMATION FOR SEQ ID NO: 2:
81   (i) SEQUENCE CHARACTERISTICS:
82       (A) LENGTH: 141 amino acids
83       (B) TYPE: amino acid
84       (C) STRANDEDNESS:
85       (D) TOPOLOGY: linear
86   (ii) MOLECULE TYPE: peptide
87   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
91   Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys
92   1           5           10           15
94   Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
95   20          25          30
97   Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
98   35          40          45
100  Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
101  50          55          60
103  Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
104  65          70          75          80
106  Ser Ala Leu Ser Asp Leu His Ala His Lys Lys Arg Val Asp Pro Val
107  85          90          95
109  Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
110  100         105         110
112  Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
113  115         120         125
115  Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
116  130         135         140

119 (2) INFORMATION FOR SEQ ID NO: 3:
121   (i) SEQUENCE CHARACTERISTICS:
122       (A) LENGTH: 438 base pairs
123       (B) TYPE: nucleic acid
124       (C) STRANDEDNESS: single
125       (D) TOPOLOGY: linear
126   (ii) MOLECULE TYPE: DNA (cDNA)
127   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
131  GTGCACCTGA CTCCTGAGGA GAAGTCTGCC GTTACTGCC TGTGGGGCAA GGTGAACGTG      60
133  GATGAAGTTG GTGGTGAGGC CTGGGCAGG CTGCTGGTGG TCTACCTTTG GACCCAGAGG      120
135  TTCITTGAGT CCTTTGGGGA TCTGTCCACT CCGTATGCTG TTAATGGGCA CCCTAAGGTG      180
137  AAGGCTCAGT GCAAGAAAGT GCTCGGTGCC TTTAGTGATG GCCTGGCTCA CCTGGACAAC      240
139  CTCGAAGGCCA CCTTTGCCAC ACTGAGTGGG CTGCACCTGT ACAAGCTGCA CGTGGATCCT      300
141  GAGAAGTTCA GCGTCTGGG CAACGTGCTG GTCTGTGTGC TGGCCCATCA CTTTGGCAAA      360
143  GAATTCACCC CACCACTGCA GGCTGCCTAT CAGAAAGTGG TGGCTGGTGT GGCTAATGCC      420
145  CTGGCCCAAC AGTATCAC                                         438

148 (2) INFORMATION FOR SEQ ID NO: 4:
150   (i) SEQUENCE CHARACTERISTICS:

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151      (A) LENGTH: 146 amino acids
152      (B) TYPE: amino acid
153      (C) STRANDEDNESS:
154      (D) TOPOLOGY: linear
155
156      (ii) MOLECULE TYPE: peptide
157
158      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
159      Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly
160      1      5      10      15
161      Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
162      20      25      30
163      Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
164      35      40      45
165      Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
166      50      55      60
167      Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn
168      65      70      75      80
169      Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu
170      85      90      95
171      His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Leu Val Cys
172      100      105      110
173      Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
174      115      120      125
175      Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
176      130      135      140
177      Tyr His
178      145
179
180      (2) INFORMATION FOR SEQ ID NO: 5:
181
182      (i) SEQUENCE CHARACTERISTICS:
183
184      (A) LENGTH: 141 amino acids
185      (B) TYPE: amino acid
186      (C) STRANDEDNESS:
187      (D) TOPOLOGY: linear
188
189      (ii) MOLECULE TYPE: peptide
190
191      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
192      Val Leu Ser Gly Glu Asp Lys Ser Asn Ile Lys Ala Ala Trp Gly Lys
193      1      5      10      15
194      Ile Gly Gly His Gly Ala Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
195      20      25      30
196      Phe Ala Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Val
197      35      40      45
198      Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
199      50      55      60
200      Ala Leu Ala Ser Ala Ala Gly His Leu Asp Asp Leu Pro Gly Ala Leu
201      65      70      75      80
202      Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
203      85      90      95
204      Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ser His
205      100      105      110
206      His Pro Ala Asp Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe

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225             115             120             125
227      Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
228             130             135             140
231 (2) INFORMATION FOR SEQ ID NO: 6:
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 146 amino acids
234 (B) TYPE: amino acid
235 (C) STRANDEDNESS:
236 (D) TOPOLOGY: linear
237 (ii) MOLECULE TYPE: peptide
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
239      Val His Leu Thr Asp Ala Glu Lys Ala Ala Val Ser Cys Leu Trp Gly
240      1             5             10             15
241      Lys Val Asn Ser Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
242      20             25             30
243      Val Val Tyr Pro Trp Thr Gln Arg Tyr Phe Asp Ser Phe Gly Asp Leu
244      35             40             45
245      Ser Ser Ala Ser Ala Ile Met Gly Asn Ala Lys Val Lys Ala His Gly
246      50             55             60
247      Lys Lys Val Ile Thr Ala Phe Asn Asp Gly Leu Asn His Leu Asp Ser
248      65             70             75
249      Leu Lys Gly Thr Phe Ala Ser Leu Ser Glu Leu His Cys Asp Lys Leu
250      85             90             95
251      His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Met Ile Val Ile
252      100            105            110
253      Val Leu Gly His His Leu Gly Lys Asp Phe Thr Pro Ala Ala Gln Ala
254      115            120            125
255      Ala Phe Gln Lys Val Val Ala Gly Val Ala Thr Ala Leu Ala His Lys
256      130            135            140
257      Tyr His
258      145
259 (2) INFORMATION FOR SEQ ID NO: 7:
260 (i) SEQUENCE CHARACTERISTICS:
261 (A) LENGTH: 141 amino acids
262 (B) TYPE: amino acid
263 (C) STRANDEDNESS:
264 (D) TOPOLOGY: linear
265 (ii) MOLECULE TYPE: peptide
266 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
267      Val Leu Ser Ala Ala Asp Lys Ala Asn Val Lys Ala Ala Trp Gly Lys
268      1             5             10             15
269      Val Gly Gly Gln Ala Gly Ala His Gly Ala Glu Ala Leu Glu Arg Met
270      20             25             30
271      Phe Leu Gly Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asn Leu
272      35             40             45
273      Ser His Gly Ser Asp Gln Val Lys Ala His Gly Gln Lys Val Ala Asp
274      50             55             60
275      Ala Leu Thr Lys Ala Val Gly His Leu Asp Asp Leu Pro Gly Ala Leu
276      65             70             75             80

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```

301      Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
302                               85          90          95
304      Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
305                               100         105         110
307      His Pro Asp Asp Phe Asn Pro Ser Val His Ala Ser Leu Asp Lys Phe
308                               115         120         125
310      Leu Ala Asn Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
311      130          135          140
314 (2) INFORMATION FOR SEQ ID NO: 8:
316 (i) SEQUENCE CHARACTERISTICS:
317 (A) LENGTH: 146 amino acids
318 (B) TYPE: amino acid
319 (C) STRANDEDNESS:
320 (D) TOPOLOGY: linear
322 (ii) MOLECULE TYPE: peptide
324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
326 Val His Leu Ser Ala Glu Glu Lys Glu Ala Val Leu Gly Leu Trp Gly
327 1          5          10          15
329 Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
330 20         25         30
332 Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
333 35         40         45
335 Ser Asn Ala Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
336 50         55         60
338 Lys Lys Val Leu Gln Ser Phe Ser Asp Gly Leu Lys His Leu Asp Asn
339 65         70         75         80
341 Leu Lys Gly Thr Phe Ala Lys Leu Ser Glu Leu His Cys Asp Gln Leu
342 85         90         95
344 His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Ile Val Val
345 100        105        110
347 Val Leu Ala Arg Arg Leu Gly His Asp Phe Asn Pro Asp Val Gln Ala
348 115        120        125
350 Ala Phe Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
351 130        135        140
353 Tyr His
354 145
356 (2) INFORMATION FOR SEQ ID NO: 9:
358 (i) SEQUENCE CHARACTERISTICS:
359 (A) LENGTH: 23 amino acids
360 (B) TYPE: amino acid
361 (C) STRANDEDNESS:
362 (D) TOPOLOGY: linear
364 (ii) MOLECULE TYPE: peptide
366 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
368 Val His Leu Ser Ala Glu Glu Lys Glu Ala Val Leu Gly Leu Trp Gly
369 1          5          10          15
371 Lys Val Asn Val Asp Glu Val
372 20
375 (2) INFORMATION FOR SEQ ID NO: 10:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/839,164

DATE: 01/22/2002

TIME: 17:02:43

Input Set : A:\09839164.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]